Amendments to the Specification:

Please delete the paragraph on page 12, lines 28-31, and replace it with the following paragraph:

Figures 24-33 are heavy chain and kappa chain cDNA and protein sequences of or for the antibodies: CEM 10.1 C3 (Fig. 24, SEQ ID NOS 62, 23, 63, & 24), CEM 10.1 G10 (Fig. 25, SEQ ID NOS 64, 25, 65, & 26), CEM 10.12 F3 (Fig. 26, SEQ ID NOS 66, 27, 67, & 28), CEM 10.12 G5 (Fig. 27, SEQ ID NOS 68, 29, 69, & 30), CEM 13.12 (Fig. 28, SEQ ID NOS 70, 31, 71, & 32), CEM 13.5 (Fig. 29, SEQ ID NOS 72, 33, 73, & 34), 2.4.4 (Fig. 30, SEQ ID NOS 74, 35, 75, & 36), 2.1.1 (Fig. 31, SEQ ID NOS 76, 37, 77, & 38), 2.3.2 (Fig. 32, SEQ ID NOS 78 & 39), and 2.6.1 (Fig. 33, SEQ ID NOS 79, 40, 80, & 41).

Please delete the paragraph on page 12/1, lines 1-4, and replace it with the following paragraph:

Figures 34-43 are heavy chain and kappa chain protein sequences of or for the antibodies: CEM 10.1 C3 (Fig. 34, SEQ ID NOS 23-24), CEM 10.1 G10 (Fig. 35, SEQ ID NOS 25-26), CEM 10.12 F3 (Fig. 36, SEQ ID NOS 27-28), CEM 10.12 G5 (Fig. 37, SEQ ID NOS 29-30), CEM 13.12 (Fig. 38, SEQ ID NOS 31-32), CEM 13.5 (Fig. 39, SEQ ID NOS 33-34), 2.4.4 (Fig. 40, SEQ ID NOS 35-36), 2.1.1 (Fig. 41, SEQ ID NOS 37-38), 2.3.2 (Fig. 42, SEQ ID NO: 39), and 2.6.1 (Fig. 43, SEQ ID NOS 40-41) showing CDR positions.

Please delete the paragraph on page 12/1, lines 5-7, and replace it with the following paragraph:

Figures 44-46 are heavy chain and kappa chain protein sequence alignments of certain of the antibodies showing alignment against the respective germline V-segment genes (Fig. 44A: SEQ ID NOS 82-84, Fig. 44B: SEQ ID NOS 85-87, Fig. 45A: SEQ ID NOS 88-90, Fig. 45B: SEQ ID NOS 91-93, Fig. 45C: SEQ ID NOS 94-96, Fig. 46: SEQ ID NOS 97-99).

Please delete the paragraph on page 12/1, lines 20-22, and replace it with the following paragraph:

Figures 50-51 provide additional detail of the cloning strategy utilized in connection with the generation of CD147-IgG2 and gp42-IgG2 fusion proteins for use in connection with the generation of surrogate antibodies for use in animal models (Fig. 50B: SEQ ID NOS 100-101, Fig. 50C: SEQ ID NOS 102-103, Fig. 50D: SEQ ID NOS 104-105).

Please delete the paragraph on page 13, line 24, to page 14, line 2, and replace it with the following paragraph:

In accordance with a third aspect of the present invention, there is provided an isolated monoclonal antibody having the following characteristics: binds to CD147; shows a binding against CEM cell lysates on Western blot similar to that provided in Figure 1; an isotype selected from the group consisting of murine IgM, murine IgG2a, murine IgG2b, murine IgG3, human IgM, human IgG1, and human IgG3; competes with ABX-CBL for binding to CD147; cross reacts with hn-RNP-k protein; binds to a consensus sequence on CD147 comprising RVRS (SEQ ID NO: 106); selectively kills activated T-cells, activated B-cells, and monocytes in a MLR assay only in the presence of complement; and is substantially non-toxic to cells expressing CD55 and CD59, with and without the presence of complement, with the proviso that the antibody is not CBL1.

Please delete the paragraph on page 14, lines 3-17, and replace it with the following paragraph:

In accordance with a fourth aspect of the present invention, there is provided a method to select an anti-CD147 antibodies for the treatment of disease, comprising: generating antibodies that bind to CD147 and that are capable of binding complement; assaying the antibodies for one or more of the following properties: competition with ABX-CBL for binding to CD147; capability to selectively kill activated T-cells, activated B-cells, and monocytes in a MLR assay only in the presence of complement; and being substantially non-toxic to cells expressing CD55 and CD59, with

and without the presence of complement, with the proviso that the antibody is not CBL1. In a preferred embodiment, the method comprises assaying the antibodies for binding to CEM cell lysates on Western blot in a manner similar to that provided in Figure 1. In another preferred embodiment, the method comprises assaying the antibodies for binding to a consensus sequence in a peptide of RXRS (SEQ ID NO: 11). In another preferred embodiment, the method comprises assaying the antibodies for cross reaction with hn-RNP-k protein. In another preferred embodiment, the method comprises assaying the antibodies for binding to a form of CD147 expressed by COS cells and *E. coli* cells.

Please delete the paragraph on page 15, lines 8-11, and replace it with the following paragraph:

In accordance with a seventh aspect of the present invention, there is provided a monoclonal antibody that binds to an epitope on CD147 comprising the consensus sequence RVRSH (SEQ ID NO: 107), wherein the antibody is not CBL1. In a preferred embodiment, the antibody is a human antibody.

Please delete the paragraph on page 15, lines 12-15, and replace it with the following paragraph:

In accordance with an eighth aspect of the present invention, there is provided an isolated peptide comprising the sequence selected from the group consisting of RXRS (SEQ ID NO: 11), RXRSH (SEQ ID NO: 13), RVRS (SEQ ID NO: 106), and RVRSH (SEQ ID NO: 107). In a preferred embodiment, the peptide is used for the generation of antibodies.

Please delete the paragraph on page 37, line 25, to page 38, line 4, and replace it with the following paragraph:

These results indicate that while the sequence within CD147 that contains the consensus sequence RXRSH (SEQ ID NO: 13) is important to the binding of the ABX-CBL antibody to CD147, it does not fully explain ABX-CBL's binding to CD147. Indeed, the data also suggests that the consensus sequence contained either in the 15-mer

peptide when bound to the plate or the reactive phage materials when tethered to the phage coat protein binds more tightly to the ABX-CBL antibody than does the free peptide in solution. Taken together, while not wishing to bound to any particular theory or mode of operation, it is possible that CD147 possesses certain conformations that are not well mimicked in the 15-mer peptide in solution. Nevertheless, the above epitopic information is important to understanding the manner in which the ABX-CBL antibody binds to CD147 and to producing other candidate molecules against CD147 as a therapeutic target.

Please delete the paragraph on page 38, lines 5-10, and replace it with the following paragraph:

It is interesting to note that in addition to the results above in connection with the presence of the RXRSH consensus sequence (SEQ ID NO: 13) within CD147, we also looked for the presence of the consensus sequence within the hn-RNP-k protein to which ABX-CBL also appears to bind. Such analyses were conducted by sequence alignment against the phage derived peptides discussed above. Two sequences were found which possessed statistically interesting matches:

Please delete the paragraph on page 47, lines 11-22, and replace it with the following paragraph:

In connection with simulating or mimicking the structural aspects of ABX-CBL binding, we expect to be able readily generate antibodies that bind to CD147 in a similar manner as ABX-CBL. With the information discussed above, we know at least three levels of detail related to ABX-CBL's binding to CD147: (i) ABX-CBL appears to bind, if not preferentially, to a form of CD147 expressed on the population of cells selected from the group consisting of activated T-cells, activated B-cells, and monocytes, (ii) ABX-CBL shows clear and specific binding to 62 KD and 35 KD molecular species on Western blot analysis, and (iii) ABX-CBL appears very specific to an epitope on CD147 (and potentially a similar epitope on hn-RNP-k protein) defined by the consensus sequence RXRSH (SEQ ID NO: 13). In addition, ABX-CBL can be utilized to "structurally"

compare, screen, or act as a functional assay for additional antibody candidates to CD147 through competition studies.

Please delete the paragraph on page 50, line 19, to page 51, line 5, and replace it with the following paragraph:

In connection with the generation of antibodies through immunization techniques, both classical and advanced immunization techniques can be used. By classical, we mean that animals can simply be immunized with the antigen, lymphocytic cells fused with myeloma cells, and hybridomas screened therefrom. By advanced, we mean that either immunization schemes can be biased or, instead of simply forming hybridomas, lymphocytic cells can be used directly to form display libraries and screened using, for example, phage or other display technologies. Such techniques are conventional in the art and are discussed in additional detail below. In connection with biasing immunizations, one can immunize with CD147, followed by immunization with peptides, such as the 15-mer peptide mentioned above. In this manner, there is a higher probability of generating antibodies that possess specificity and affinity for selected epitopes for example. Thus, it is expected that antibodies having specificity for the RXRSH consensus sequence (SEQ ID NO: 13) in CD147, as discussed above, can be more readily generated. It will be appreciated that such immunization techniques can be utilized in connection with standard fusions and screening procedures or advanced screening procedures. Another set of advanced immunization techniques are related to techniques of antigen presentation (i.e., DEC systems) and techniques to augment the immune response (i.e., CD140 systems) in the animal in which the immunization is being undertaken.

Please delete the paragraph on page 78, lines 5-16, and replace it with the following paragraph:

These results indicate that while the sequence within CD147 that contains the consensus sequence RXRSH (SEQ ID NO: 13) is important to the binding of the ABX-CBL antibody to CD147, it does not fully explain ABX-CBL's binding to CD147. Indeed, the data also suggests that the consensus sequence contained either in the 15-mer

peptide when bound to the plate or the reactive phage materials when tethered to the phage coat protein binds more tightly to the ABX-CBL antibody than does the free peptide in solution. Taken together, while not wishing to bound to any particular theory or mode of operation, it is possible that CD147 possesses certain conformations that are not well mimicked in the 15-mer peptide in solution. Nevertheless, the above epitopic information is important to understanding the manner in which the ABX-CBL antibody binds to CD147 and to producing other candidate molecules against CD147 as a therapeutic target.

Please delete the paragraph on page 78, lines 17-22, and replace it with the following paragraph:

It is interesting to note that in addition to the results above in connection with the presence of the RXRSH consensus sequence (SEQ ID NO: 13) within CD147, we also looked for the presence of the consensus sequence within the hn-RNP-k protein to which ABX-CBL also appears to bind. Such analyses were conducted by sequence alignment against the phage derived peptides discussed above. Two sequences were found which possessed statistically interesting matches:

Please replace the Sequence Listing with the substitute Sequence Listing (pages 1-44) submitted herewith.